

SEQUENCE LISTING

<110> Bejanin, Stephan
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<141> 2001-10-15

<150> 2001-08-10

<151> 60/311,305

<150> 2001-08-24

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tgtgtgggcg tgggggcagt cttgcccagg ctggtctgga actcctggcc tcaagtgatc 180
ctcctccgtc aagatatgaa caggagtaca gctgtgtagt aaag atg cct tct ggt 236
Met Pro Ser Gly

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gaa ttt gca cgt ata tgc cga gat ctc agc cat att gga gat gct gtt 284
Glu Phe Ala Arg Ile Cys Arg Asp Leu Ser His Ile Gly Asp Ala Val
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Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu
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Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln Thr Ser Asn Val Asp Lys
40 45 50

gag gag gaa gct gtt acc ata gag atg aat gaa cca gtt caa cta act 428
Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro Val Gln Leu Thr
55 60 65

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Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser
70 75 80

tca acg gtg aca ctc agt atg tct gca gat gta ccc ctt gtt gta gag 524
Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu
85 90 95 100

tat aaa att gcg gat atg gga cac tta aaa tac tac ttg gct ccc aag 572
Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys
105 110 115

atc gag gat gaa gaa gga tct taggcattct taaaattcaa gaaaataaaa 623
Ile Glu Asp Glu Glu Gly Ser
120

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35 40 45

Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro
50 55 60

Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala
65 70 75 80

Thr Pro Leu Ser Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro
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 acc tta aat att aaa act cgg aaa cca gct ctc gtc tcc gtt ggc tct 162
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 Ala Ser Ser Ser Trp Trp Arg Val Met Ala Leu Ile Leu Leu Ile Leu
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 Cys Val Gly Met Val Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val
 45 50 55
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 60 65 70
 ctg caa caa tta gca aag cgc ttc tgt caa tat gtg gta aaa caa tca 354
 Leu Gln Gln Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser
 75 80 85
 gaa cta aag ggc act ttc aaa ggt cat aaa tgc agc ccc tgt gac aca 402
 Glu Leu Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr
 90 95 100
 aac tgg aga tat tat gga gat agc tgc tat ggg ttc ttc agg cac aac 450
 Asn Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn

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Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala Thr							
125	130	135					
ctc ctg aag att gac aac cgg aac att gtg gag tac atc aaa gcc agg	546						
Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys Ala Arg							
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act cat tta att cgt tgg gtc gga tta tct cgc cag aag tcg aat gag	594						
Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys Ser Asn Glu							
155	160	165					
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Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu Asn Met Phe Glu							
170	175	180					
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Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys Ala Tyr Phe His Asn							
185	190	195	200				
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Gly Lys Met His Pro Thr Phe Cys Glu Asn Lys His Tyr Leu Met Cys							
205	210	215					
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35 40 45
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50 55 60
Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe
65 70 75 80
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85 90 95
His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser
100 105 110
Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln
115 120 125
Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp Asn Arg Asn
130 135 140
Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg Trp Val Gly
145 150 155 160
Leu Ser Arg Gln Lys Ser Asn Glu Val Trp Lys Trp Glu Asp Gly Ser
165 170 175
Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly Lys Gly Asn

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aacacaccaa ggaaaattaa tataggaaaa atttaaaaag ttattagagg actgaaaata 180
taaaaatgga acactgaaag acacagagtt tttattttca gcactgcagc tctg atg 237
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gtc cag ctc cac cag gac aca gat ccc cag atc cct aaa ggt cag cca 285
Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln Pro
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tgc acc ctg aac agc tca gag gga gga gcc agg cca gca gtg cct cac 333
Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro His
      20      25      30
acc ttg ttc tct tct gct cta gac aga tgg ctc cat aat gac agc ttc 381
Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser Phe
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ata atg gca gtg ggt gag ccc ctg gtg cac atc agg gtc act ctt ctg 429
Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu Leu
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Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln Ala
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Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu Lys
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Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser Tyr
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130						135					140				145	
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His	Ala	Leu	Leu	Gln	Asp	Gln	Pro	Phe	Ile	Gln	Asp	Asp	Cys	Tyr	Tyr	
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Glu	Ile	Lys	Pro	Ile	Ser	Val	Ser	Ala	Thr	Phe	Glu	His	Leu	Val	Tyr	
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Thr	Glu	Glu	Lys	Ile	Ala	His	Gln	Met	Glu	Leu	Gln	Leu	Ser	Tyr	Asn	
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Phe	Thr	Leu	Lys	Gln	Ser	Ser	Phe	Val	Gly	Trp	Trp	Thr	His	Gln	Arg	
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Leu	Asp	Asn	Val	Leu	Glu	Asp	Phe	Ser	Ile	Trp	Lys	Asn	Tyr	Asn	Leu	
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Pro	Phe	Asn	Thr	Gly	Val	Asp	Val	Phe	Glu	Asp	Asn	Arg	Leu	Val	Val	
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Asp	Pro	Cys	Cys	Leu	Leu	Asn	Cys	Thr	Leu	His	Pro	Gly	Ala	Ala	Cys	
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agt	aaa	gaa	gat	gaa	gaa	gga	taagagaaat gggaaaaaga aggagactaa									2592
Ser	Lys	Glu	Asp	Glu	Glu	Gly										
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His	Thr	Leu	Phe	Ser	Ser	Ala	Leu	Asp	Arg	Trp	Leu	His	Asn	Asp	Ser
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Phe	Ile	Met	Ala	Val	Gly	Glu	Pro	Leu	Val	His	Ile	Arg	Val	Thr	Leu
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Leu	Leu	Leu	Trp	Phe	Gly	Met	Phe	Leu	Ser	Ile	Ser	Gly	His	Ser	Gln
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Ala	Arg	Pro	Ser	Gln	Tyr	Phe	Thr	Ser	Pro	Glu	Val	Val	Ile	Pro	Leu
				85					90					95	
Lys	Val	Ile	Ser	Arg	Gly	Arg	Gly	Ala	Lys	Ala	Pro	Gly	Trp	Leu	Ser
			100					105					110		
Tyr	Ser	Leu	Arg	Phe	Gly	Gly	Gln	Arg	Tyr	Ile	Val	His	Met	Arg	Val
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Gln	His	Ala	Leu	Leu	Gln	Asp	Gln	Pro	Phe	Ile	Gln	Asp	Asp	Cys	Tyr

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Tyr	His	Gly	Tyr	Val	Glu	Gly	Val	Pro	Glu	Ser	Leu	Val	Ala	Leu	Ser
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Thr	Cys	Ser	Gly	Gly	Phe	Leu	Gly	Met	Leu	Gln	Ile	Asn	Asp	Leu	Val
				180					185					190	
Tyr	Glu	Ile	Lys	Pro	Ile	Ser	Val	Ser	Ala	Thr	Phe	Glu	His	Leu	Val
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Tyr	Lys	Ile	Asp	Ser	Asp	Asp	Thr	Gln	Phe	Pro	Pro	Met	Arg	Cys	Gly
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Leu	Thr	Glu	Glu	Lys	Ile	Ala	His	Gln	Met	Glu	Leu	Gln	Leu	Ser	Tyr
225					230					235					240
Asn	Phe	Thr	Leu	Lys	Gln	Ser	Ser	Phe	Val	Gly	Trp	Trp	Thr	His	Gln
				245					250					255	
Arg	Phe	Val	Glu	Leu	Val	Val	Val	Val	Asp	Asn	Ile	Arg	Tyr	Leu	Phe
				260					265					270	
Ser	Gln	Ser	Asn	Ala	Thr	Thr	Val	Gln	His	Glu	Val	Phe	Asn	Val	Val
				275					280					285	
Asn	Ile	Val	Asp	Ser	Phe	Tyr	His	Pro	Leu	Glu	Val	Asp	Val	Ile	Leu
				290					295					300	
Thr	Gly	Ile	Asp	Ile	Trp	Thr	Ala	Ser	Asn	Pro	Leu	Pro	Thr	Ser	Gly
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Asp	Leu	Asp	Asn	Val	Leu	Glu	Asp	Phe	Ser	Ile	Trp	Lys	Asn	Tyr	Asn
				325					330					335	
Leu	Asn	Asn	Arg	Leu	Gln	His	Asp	Val	Ala	His	Leu	Phe	Ile	Lys	Asp
				340					345					350	
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Asn	Pro	Phe	Asn	Thr	Gly	Val	Asp	Val	Phe	Glu	Asp	Asn	Arg	Leu	Val
				370					375					380	
Val	Phe	Ala	Ile	Thr	Leu	Gly	His	Glu	Leu	Gly	His	Asn	Leu	Gly	Met
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Gln	His	Asp	Thr	Gln	Trp	Cys	Val	Cys	Glu	Leu	Gln	Trp	Cys	Ile	Met
				405					410					415	
His	Ala	Tyr	Arg	Lys	Val	Thr	Thr	Lys	Phe	Ser	Asn	Cys	Ser	Tyr	Ala
				420					425					430	
Gln	Tyr	Trp	Asp	Ser	Thr	Ile	Ser	Ser	Gly	Leu	Cys	Ile	Gln	Pro	Pro
				435					440					445	
Pro	Tyr	Pro	Gly	Asn	Ile	Phe	Arg	Leu	Lys	Tyr	Cys	Gly	Asn	Leu	Val
				450					455					460	
Val	Glu	Glu	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Thr	Ile	Arg	Gln	Cys	Ala
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Lys	Asp	Pro	Cys	Cys	Leu	Leu	Asn	Cys	Thr	Leu	His	Pro	Gly	Ala	Ala
				485					490					495	
Cys	Ala	Phe	Gly	Ile	Cys	Cys	Lys	Asp	Cys	Lys	Phe	Leu	Pro	Ser	Gly
				500					505					510	
Thr	Leu	Cys	Arg	Gln	Gln	Val	Gly	Glu	Cys	Asp	Leu	Pro	Glu	Trp	Cys
				515					520					525	
Asn	Gly	Thr	Ser	His	Gln	Cys	Pro	Asp	Asp	Val	Tyr	Val	Gln	Asp	Gly
				530					535					540	
Ile	Ser	Cys	Asn	Val	Asn	Ala	Phe	Cys	Tyr	Glu	Lys	Thr	Cys	Asn	Asn
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His	Asp	Ile	Gln	Cys	Lys	Glu	Ile	Phe	Gly	Gln	Asp	Ala	Arg	Ser	Ala
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Ser	Gln</														

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His Cys Gly Ile Val Gly Thr Thr Tyr Val Lys Cys Trp Thr Pro Asp
      595      600      605
Ile Met Cys Gly Arg Val Gln Cys Glu Asn Val Gly Val Ile Pro Asn
      610      615      620
Leu Ile Glu His Ser Thr Val Gln Gln Phe His Leu Asn Asp Thr Thr
      625      630      635      640
Cys Trp Gly Thr Asp Tyr His Leu Gly Met Ala Ile Pro Asp Ile Gly
      645      650      655
Glu Val Lys Asp Gly Thr Val Cys Gly Pro Glu Lys Ile Cys Ile Arg
      660      665      670
Lys Lys Cys Ala Ser Met Val His Leu Ser Gln Ala Cys Gln Pro Lys
      675      680      685
Thr Cys Asn Met Arg Gly Ile Cys Asn Asn Lys Gln His Cys His Cys
      690      695      700
Asn His Glu Trp Ala Pro Pro Tyr Cys Lys Asp Lys Gly Tyr Gly Gly
      705      710      715      720
Ser Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn
      725      730      735
Val Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu
      740      745      750
Val Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr
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Lys Ser Lys Glu Asp Glu Glu Gly
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<212> DNA
<213> Homo sapiens

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<220>
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<220>
<221> polyA_site
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gcagggcaaa cactgaggtc aactacaagc cacaggcccc ttccccagcc tcagttcaca 180
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ccaaggcaga ggagcccata gcc atg agg agc ctc ggg gcc ctg ctc ttg ctg 293
Met Arg Ser Leu Gly Ala Leu Leu Leu Leu
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ctg agc gcc tgc ctg gcg gtg agc gct ggc cct gtg cca acg ccg ccc 341
Leu Ser Ala Cys Leu Ala Val Ser Ala Gly Pro Val Pro Thr Pro Pro
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Asp Asn Ile Gln Val Gln Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly
10 15 20
aag tgg tac aac ctg gcc atc ggt tcc acc tgc ccc tgg ctg aag aag 437
Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys
25 30 35
atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga gag ggc gct 485
Ile Met Asp Arg Met Thr Val Ser Thr Leu Val Leu Gly Glu Gly Ala
40 45 50 55
aca gag gcg gag atc agc atg acc agc act cgt tgg cgg aaa ggt gtc 533
Thr Glu Ala Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Lys Gly Val
60 65 70
tgt gag gag acg tct gga gct tat gag aaa aca gat act gat ggg aag 581
Cys Glu Glu Thr Ser Gly Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys
75 80 85
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Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Met Glu Ser Tyr Val
90 95 100
gtc cac acc aac tat gat gag tat gcc att ttc ctg acc aag aaa ttc 677
Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe
105 110 115
agc cgc cat cat gga ccc acc att act gcc aag ctc tac ggg cgg gcg 725
Ser Arg His His Gly Pro Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala
120 125 130 135
ccg cag ctg agg gaa act ctc ctg cag gac ttc aga gtg gtt gcc cag 773
Pro Gln Leu Arg Glu Thr Leu Leu Gln Asp Phe Arg Val Val Ala Gln
140 145 150
ggc gtg ggc atc cct gag gac tcc atc ttc acc atg gct gac cga ggt 821
Gly Val Gly Ile Pro Glu Asp Ser Ile Phe Thr Met Ala Asp Arg Gly
155 160 165
gaa tgt gtc cct ggg gag cag gaa cca gag ccc atc tta atc ccg aga 869
Glu Cys Val Pro Gly Glu Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg
170 175 180
gtc cgg agg gct gct acc cca aga aga gga agg atc agg ggg tgg gca 917
Val Arg Arg Ala Ala Thr Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala
185 190 195
act ggt aac tgaagtcacc aagaaagaag attcctgccca gctgggctac 966
Thr Gly Asn
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1436

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<213> Homo sapiens

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<222> 1..19

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Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala
 15 20 25
Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr
30 35 40 45
Val Ser Thr Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser
 50 55 60
Met Thr Ser Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly
 65 70 75
Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser
 80 85 90
Lys Trp Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp
 95 100 105
Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro
110 115 120 125
Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr
 130 135 140
Leu Leu Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu
 145 150 155
Asp Ser Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu
 160 165 170
Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Ala Thr
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Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala Thr Gly Asn
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<220>
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 Met Gln Arg Leu Gln Val Val
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 ctg ggc cac ctg agg ggt ccg gcc gat tcc ggc tgg atg ccg cag gcc 161
 Leu Gly His Leu Arg Gly Pro Ala Asp Ser Gly Trp Met Pro Gln Ala
 -25 -20 -15
 gcg cct tgc ctg agc ggt gcc ccg cag gcc tcg gcc gcg gac gtg gtg 209
 Ala Pro Cys Leu Ser Gly Ala Pro Gln Ala Ser Ala Ala Asp Val Val
 -10 -5 1
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 Val Val His Gly Arg Arg Thr Ala Ile Cys Arg Ala Gly Arg Gly Gly
 5 10 15 20
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 Phe Lys Asp Thr Thr Pro Asp Glu Leu Leu Ser Ala Val Met Thr Ala
 25 30 35
 gtt ctc aag gac gtg aat ctg agg ccg gaa cag ctg ggg gac atc tgt 353
 Val Leu Lys Asp Val Asn Leu Arg Pro Glu Gln Leu Gly Asp Ile Cys
 40 45 50
 gtc gga aat gtg ctg cag cct ggg gcc ggg gca atc atg gcc cga atc 401
 Val Gly Asn Val Leu Gln Pro Gly Ala Gly Ala Ile Met Ala Arg Ile
 55 60 65
 gcc cag ttt ctg agt gac atc ccg gag act gtg cct ttg tcc act gtc 449
 Ala Gln Phe Leu Ser Asp Ile Pro Glu Thr Val Pro Leu Ser Thr Val
 70 75 80
 aat aga cag tgt tcg tcg ggg cta cag gca gtg gcc agc ata gca ggg 497
 Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Ser Ile Ala Gly
 85 90 95 100
 tgg agt cca tgt ccc tgg ctg aca gag gga acc ctg gaa ata tta ctt 545
 Trp Ser Pro Cys Pro Trp Leu Thr Glu Gly Thr Leu Glu Ile Leu Leu
 105 110 115
 cgc gct tgatggagaa ggagaaggcc agagattgcc tgattcctat ggggataacc 601
 Arg Ala
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 aagtagaagt gggagggctg ggatctcctc atccccaccc cgatgccttc ttaccccaac 1021
 agtttgcgcc taggaaactc tagccaggtg agtgatgggg cagctgccat cctgctggcc 1081

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ctttagctgt gcaagataaa agcagcctgg gtcacccagg ccacaaggcc atgggttaatt 2041
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 <213> Homo sapiens

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Ala	Ser	Ala	Ala	Asp	Val	Val	Val	Val	His	Gly	Arg	Arg	Thr	Ala	Ile
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Cys	Arg	Ala	Gly	Arg	Gly	Gly	Phe	Lys	Asp	Thr	Thr	Pro	Asp	Glu	Leu
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Glu	Gln	Leu	Gly	Asp	Ile	Cys	Val	Gly	Asn	Val	Leu	Gln	Pro	Gly	Ala
				50					55					60	
Gly	Ala	Ile	Met	Ala	Arg	Ile	Ala	Gln	Phe	Leu	Ser	Asp	Ile	Pro	Glu
			65				70					75			
Thr	Val	Pro	Leu	Ser	Thr	Val	Asn	Arg	Gln	Cys	Ser	Ser	Gly	Leu	Gln
		80				85						90			
Ala	Val	Ala	Ser	Ile	Ala	Gly	Trp	Ser	Pro	Cys	Pro	Trp	Leu	Thr	Glu
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<210> 11
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Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser				
	150	155	160	
gtt acc agc atc ctc cat atc aaa gac cct aag aat cag gtg ggg aag				809
Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys				
	165	170	175	180
gag gtg atc tgc cag gtg ctg cac ctg ggg act gtg acc gac ttt aag				857
Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val Thr Asp Phe Lys				
	185	190	195	
caa acc gtc aac aaa ggc tat tgg ttt tca gtt ccg cta ttg cta agc				905
Gln Thr Val Asn Lys Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser				
	200	205	210	
att gtt tcc ctg gta att ctt ctc gtc cta atc tca atc tta ctg tac				953
Ile Val Ser Leu Val Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr				
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Trp Lys Arg His Arg Asn Gln Asp Arg Glu Pro				
	230	235		
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gaatccttgg tttcactgct gttcttcatg tgcttctatg agatttactc caacacaa				1666
aggactgaat ttattgtgaa gtaacattgg caatcttaac ttattcattt aacttatttt				1726
tatagctaga taaatattgt tagtcttaga caatagctca cattttttga gaagcatgcc				1786
ctccctgtcc atttgtctta taacatgacc cagccctatt ttacgtcatt ctaaattcag				1846
cctcatataa tgaaaataca ttatgaaaac agatgttttag gagatttcct gtatagcagt				1906
cagccaattc atatgctttg tctctgctgg cttctttttc catgctgtta cttttcccaa				1966
tagcagagga ggcaaatatg agcatacaat ccctttgttc taaagatatt gttccagcta				2026
gtggaatgat gttgaatctt taataacat aattagttgc tttttcagta tcttctgctt				2086
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gatatttata tatatatata tagcaagatt ttcatgtgtt atttaattct gtattgtttc				2206
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<210> 12
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 <212> PRT
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<220>
 <221> SIGNAL
 <222> 1..23

<400> 12

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-5 1 5
Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys Cys Ser Leu Gln Asn
10 15 20 25
Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys Lys Lys Ala Val Ser
30 35 40
Pro Glu Asn Met Val Thr Phe Ser Glu Asn His Gly Val Val Ile Gln
45 50 55
Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln Leu Gly Leu Gln Asn
60 65 70
Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu Asp Glu Gly Cys Tyr
75 80 85
Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys Ile Ser Gly Thr Ala
90 95 100 105
Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser Leu His Tyr Lys Phe
110 115 120
Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala Thr Ala Arg Pro Ala
125 130 135
Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly Ile Glu Asn Ser Thr
140 145 150
Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser Val Thr Ser Ile Leu
155 160 165
His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys Glu Val Ile Cys Gln
170 175 180 185
Val Leu His Leu Gly Thr Val Thr Asp Phe Lys Gln Thr Val Asn Lys
190 195 200
Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser Ile Val Ser Leu Val
205 210 215
Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr Trp Lys Arg His Arg
220 225 230
Asn Gln Asp Arg Glu Pro
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<210> 13
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<220>
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<222> 1558..1563

<220>

<221> polyA_site

<222> 1582..1597

<400> 13

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Met Glu Arg Met Leu Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala	
-20 -15 -10	
ggg ttc tgc cct gct gtc ctc tgc cac cct aac agc cca ctt gac gag	158
Gly Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu	
-5 1 5	
gag aat ctg acc cag gag aac caa gac cga ggg aca cac gtg gac ctc	206
Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu	
10 15 20	
gga tta gcc tcc gcc aac gtg gac ttc gct ctc agc ctg tac aag cag	254
Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln	
25 30 35 40	
tta gtc ctg aag gcc cct gat aag aat gtc atc ttc tcc cca ctg agc	302
Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser	
45 50 55	
atc tcc acc gcc ttg gcc ttc ctg tct ctg ggg gcc cat aat acc acc	350
Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr	
60 65 70	
ctg aca gag att ctc aaa ggc ctc aag ttc aac ctc acg gag act tct	398
Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser	
75 80 85	
gag gca gaa att cac cag agc ttc cag cac ctc ctg cgc acc ctc aat	446
Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn	
90 95 100	
cag tcc agc gat gag ctg cag ctg agt atg gga aat gcc atg ttt gtc	494
Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val	
105 110 115 120	
aaa gag caa ctc agt ctg ctg gac agg ttc acg gag gat gcc aag agg	542
Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg	
125 130 135	
ctg tat ggc tcc gag gcc ttt gcc act gac ttt cag gac tca gct gca	590
Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala	
140 145 150	
gct aag aag ctc atc aac gac tac gtg aag aat gga act agg ggg aaa	638
Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys	
155 160 165	
atc aca gat ctg atc aag gac ctt gac tcg cag aca atg atg gtc ctg	686
Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu	
170 175 180	
gtg aat tac atc ttc ttt aaa gcc aaa tgg gag atg ccc ttt gac ccc	734
Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro	
185 190 195 200	
caa gat act cat cag tca agg ttc tac ttg agc aag aaa aag tgg gta	782
Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val	
205 210 215	
atg gtg ccc atg atg agt ttg cat cac ctg act ata cct tac ttc cgg	830

09784610101

Met	Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	Pro	Tyr	Phe	Arg			
			220			225			230									
gac	gag	gag	ctg	tcc	tgc	acc	gtg	gtg	gag	ctg	aag	tac	aca	ggc	aat	878		
Asp	Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn			
			235			240			245									
gcc	agc	gca	ctc	ttc	atc	ctc	cct	gat	caa	gac	aag	atg	gag	gaa	gtg	926		
Ala	Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val			
			250			255			260									
gaa	gcc	atg	ctg	ctc	cca	gag	acc	ctg	aag	cgg	tgg	aga	gac	tct	ctg	974		
Glu	Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu			
265				270			275						280					
gag	ttc	aga	gag	ata	ggg	gag	ctc	tac	ctg	cca	aag	ttt	tcc	atc	tcg	1022		
Glu	Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser			
			285			290			295									
agg	gac	tat	aac	ctg	aac	gac	ata	ctt	ctc	cag	ctg	ggc	att	gag	gaa	1070		
Arg	Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	Gly	Ile	Glu	Glu			
			300			305			310									
gcc	ttc	acc	agc	aag	gct	gac	ctg	tca	ggg	atc	aca	ggg	gcc	agg	aac	1118		
Ala	Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn			
			315			320			325									
cta	gca	gtc	tcc	cag	gtg	gtc	cat	aag	gct	gtg	ctt	gat	gta	ttt	gag	1166		
Leu	Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu			
			330			335			340									
gag	ggc	aca	gaa	gca	tct	gct	gcc	aca	gca	gtc	aaa	atc	acc	ctc	ctt	1214		
Glu	Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu			
345				350			355						360					
tct	gca	tta	gtg	gag	aca	agg	acc	att	gtg	cgt	ttc	aac	agg	ccc	ttc	1262		
Ser	Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe			
			365			370			375									
ctg	atg	atc	att	gtc	cct	aca	gac	acc	cag	aac	atc	ttc	ttc	atg	agc	1310		
Leu	Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser			
			380			385			390									
aaa	gtc	acc	aat	ccc	aag	caa	gcc	tag	agc	ttg	c	cat	caag	cag	tggggctctc	1364		
Lys	Val	Thr	Asn	Pro	Lys	Gln	Ala											
			395			400												
agtaaggaac			ttggaatgca			agctggatgc			ctgggtctct			gggcacagcc			tgccccctgt			1424
gcaccgagtg			gccatggcat			gtgtggccct			gtctgcttat			ccttggaagg			tgacagcgat			1484
tccctgtgta			gctctcacat			gcacaggggc			ccatggactc			ttcagtctgg			agggtcctgg			1544
gcctcctgac			agcaataaat			aatttcgttg			gacacgcaaa			aaaaaaaaaa			aaa			1597

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<211> 423
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> 1..23
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      -20                      -15                      -10
Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
      -5                      1                      5

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Asn	Leu	Thr	Gln	Glu	Asn	Gln	Asp	Arg	Gly	Thr	His	Val	Asp	Leu	Gly
10					15					20					25
Leu	Ala	Ser	Ala	Asn	Val	Asp	Phe	Ala	Leu	Ser	Leu	Tyr	Lys	Gln	Leu
				30					35					40	
Val	Leu	Lys	Ala	Pro	Asp	Lys	Asn	Val	Ile	Phe	Ser	Pro	Leu	Ser	Ile
			45					50					55		
Ser	Thr	Ala	Leu	Ala	Phe	Leu	Ser	Leu	Gly	Ala	His	Asn	Thr	Thr	Leu
		60					65					70			
Thr	Glu	Ile	Leu	Lys	Gly	Leu	Lys	Phe	Asn	Leu	Thr	Glu	Thr	Ser	Glu
	75					80					85				
Ala	Glu	Ile	His	Gln	Ser	Phe	Gln	His	Leu	Leu	Arg	Thr	Leu	Asn	Gln
90					95					100					105
Ser	Ser	Asp	Glu	Leu	Gln	Leu	Ser	Met	Gly	Asn	Ala	Met	Phe	Val	Lys
				110					115					120	
Glu	Gln	Leu	Ser	Leu	Leu	Asp	Arg	Phe	Thr	Glu	Asp	Ala	Lys	Arg	Leu
			125					130					135		
Tyr	Gly	Ser	Glu	Ala	Phe	Ala	Thr	Asp	Phe	Gln	Asp	Ser	Ala	Ala	Ala
		140					145					150			
Lys	Lys	Leu	Ile	Asn	Asp	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Gly	Lys	Ile
	155					160					165				
Thr	Asp	Leu	Ile	Lys	Asp	Leu	Asp	Ser	Gln	Thr	Met	Met	Val	Leu	Val
170					175					180					185
Asn	Tyr	Ile	Phe	Phe	Lys	Ala	Lys	Trp	Glu	Met	Pro	Phe	Asp	Pro	Gln
				190					195					200	
Asp	Thr	His	Gln	Ser	Arg	Phe	Tyr	Leu	Ser	Lys	Lys	Lys	Trp	Val	Met
			205					210					215		
Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	Pro	Tyr	Phe	Arg	Asp
		220					225					230			
Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn	Ala
	235					240					245				
Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val	Glu
250					255					260					265
Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu	Glu
				270					275					280	
Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser	Arg
			285					290					295		
Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	Gly	Ile	Glu	Glu	Ala
		300					305					310			
Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn	Leu
	315					320					325				
Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu	Glu
330					335					340					345
Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu	Ser
				350					355				360		
Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe	Leu
			365					370					375		
Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser	Lys
		380					385					390			
Val	Thr	Asn	Pro	Lys	Gln	Ala									
	395					400									

<210> 15
 <211> 1397
 <212> DNA


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Val Pro Val Ser Gln Lys Tyr Glu Leu Gly Ala Ala Leu Tyr Ile Gly
      155      160      165
tgg gcg gcc acc gcg ctg ctc atg gta ggc ggc tgc ctc ttg tgc tgc 701
Trp Ala Ala Thr Ala Leu Leu Met Val Gly Gly Cys Leu Leu Cys Cys
      170      175      180
ggc gcc tgg gtc tgc acc ggc cgt ccc gac ctc agc ttc ccc gtg aag 749
Gly Ala Trp Val Cys Thr Gly Arg Pro Asp Leu Ser Phe Pro Val Lys
      185      190      195
tac tca gcg ccg cgg cgg ccc acg gcc acc ggc gac aac gac aag aag 797
Tyr Ser Ala Pro Arg Arg Pro Thr Ala Thr Gly Asp Asn Asp Lys Lys
200      205      210      215
aac tac gtc tgagggcgct gggcacggcc gggcccctcc tgccagccac 846
Asn Tyr Val
gcttgcgagg cggttgataa gcttggggag ccccgcatgg accgcggctt ccgcccgggta 906
gcgcgggcgcg caggcttctc ggaacgtccg gctctgcgcc ccgacgcggc tcctggatcc 966
gctcctgcct gcgcccgcag ctgaccttct cctgccacta gcccggccct gcccttaaca 1026
gacggaatga agtttctctt tctgtgcgcg gcgctgtttc cataggcaga gcgggtgtca 1086
gactgaggat ttcgcttccc ctccaagacg ctgggggtct tggtctgtgc cttacttccc 1146
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ggacctcccg gtctcactcc agcatctccc caggcaaggc ttgtgggcac cggagcttga 1326
gagagggcgg gagtggaag gctaagaatc tgcttagtaa atggtttgaa ctctgaaaaa 1386
aaaaaaaaa a 1397

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<210> 16
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 16

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Met Gly Ser Ala Ala Leu Glu Ile Leu Gly Leu Val Leu Cys Leu Val
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Gly Trp Gly Gly Leu Ile Leu Ala Cys Gly Leu Pro Met Trp Gln Val
      20      25      30
Thr Ala Phe Leu Asp His Asn Ile Val Thr Ala Gln Thr Thr Trp Lys
      35      40      45
Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly His Met Gln Cys
      50      55      60
Lys Val Tyr Asp Ser Val Leu Ala Leu Ser Thr Glu Val Gln Ala Ala
65      70      75      80
Arg Ala Leu Thr Val Ser Ala Val Leu Leu Ala Phe Val Ala Leu Phe
      85      90      95
Val Thr Leu Ala Gly Ala Gln Cys Thr Thr Cys Val Ala Pro Gly Pro
      100      105      110
Ala Lys Ala Arg Val Ala Leu Thr Gly Gly Val Leu Tyr Leu Phe Cys
      115      120      125
Gly Leu Leu Ala Leu Val Pro Leu Cys Trp Phe Ala Asn Ile Val Val
      130      135      140
Arg Glu Phe Tyr Asp Pro Ser Val Pro Val Ser Gln Lys Tyr Glu Leu
145      150      155      160
Gly Ala Ala Leu Tyr Ile Gly Trp Ala Ala Thr Ala Leu Leu Met Val
      165      170      175

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          100          105          110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
          115          120          125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
          130          135          140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
          145          150          155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
          160          165          170
gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
caccccaatg ggaccaccct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaaaaaa 772
aaaaaaaaaa 782

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<210> 18
 <211> 170
 <212> PRT
 <213> Homo sapiens

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<400> 18
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
1          5          10          15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
          20          25          30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
          35          40          45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
          50          55          60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65          70          75          80
Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
          85          90          95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
          100          105          110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
          115          120          125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
          130          135          140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145          150          155          160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
          165          170

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<210> 19
 <211> 789
 <212> DNA
 <213> Homo sapiens

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<222> 1..62

<220>

<221> CDS

<222> 63..572

<220>

<221> 3'UTR

<222> 573..789

<220>

<221> polyA_signal

<222> 750..755

<220>

<221> polyA_site

<222> 774..789

<400> 19

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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt ttg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652

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cacccaatg ggaccaccct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactct 772
caaaaaaaaa aaaaaaa 789

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<212> PRT
<213> Homo sapiens

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20 25 30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35 40 45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50 55 60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65 70 75 80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85 90 95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100 105 110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115 120 125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130 135 140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145 150 155 160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165 170

<210> 21
<211> 555
<212> DNA
<213> Homo sapiens

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<222> 1..85

<220>
<221> CDS
<222> 86..403

<220>
<221> 3'UTR
<222> 404..555

<220>
<221> polyA_signal
<222> 504..509

<211> 1726
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..414

<220>
 <221> CDS
 <222> 415..1653

<220>
 <221> 3'UTR
 <222> 1654..1726

<220>
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 <222> 1688..1726

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 cgcgtcgggt ggggcgggaa taaagttttt ccaacccagt ttggggagag ggctggatgg 180
 gaaggaccct ccctgctgca gacttcatgg caggctgcac tgtgtcccct cggctccacg 240
 gctgcccccg gggcgctgct ttcgggtttt ctttctagaa tctctggtct gctgctgtgc 300
 agatggacct gccggcactg ctgtcagaag tgctacgagt ccagctgttg ccagtcaagt 360
 gaggatgaag ttgaaattct gggacctttc cctgctcaga cccctccctg gctg atg 417
 Met
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 gcc agc cgg agc agt gac aag gat ggt gac tct gtc cac acg gcc agc 465
 Ala Ser Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser
 5 10 15
 gaa gtc ccg ctg acc cca cgg acc aat tcc ccg gat gga aga cgc tcg 513
 Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser
 20 25 30
 tcc tca gac aca tcc aag tct aca tac agc ctg acg cgg agg att tcg 561
 Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser
 35 40 45
 agt ctt gag tca aga cgt ccc agc tct cca ctc atc gat att aaa ccc 609
 Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro
 50 55 60 65
 atc gag ttt ggc gtt ctc agc gcc aag aag gag ccc atc caa cct tcg 657
 Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser
 70 75 80
 gtg ctc aga cgg acc tat aac ccc gac gac tat ttc agg aag ttc gaa 705
 Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu
 85 90 95
 ccc cac ctg tac tcc ctc gac tcc aac agc gac gat gtg gac tct ctg 753
 Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu
 100 105 110
 aca gac gag gag atc ctg tcc aag tac cag ctg ggc atg cag cac ttc 801
 Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His Phe
 115 120 125

agc	act	cag	tac	gac	ctg	ctg	cac	aac	cac	ctc	acc	gtg	cgc	gtg	atc	849
Ser	Thr	Gln	Tyr	Asp	Leu	Leu	His	Asn	His	Leu	Thr	Val	Arg	Val	Ile	
130					135					140					145	
gag	gcc	agg	gac	ctg	cca	cct	ccc	atc	tcc	cac	gat	ggc	tcg	cgc	cag	897
Glu	Ala	Arg	Asp	Leu	Pro	Pro	Pro	Ile	Ser	His	Asp	Gly	Ser	Arg	Gln	
				150					155					160		
gac	atg	gcg	cac	tcc	aac	ccc	tac	gtc	aag	atc	tgt	ctc	ctg	cca	gac	945
Asp	Met	Ala	His	Ser	Asn	Pro	Tyr	Val	Lys	Ile	Cys	Leu	Leu	Pro	Asp	
			165					170					175			
cag	aag	aac	tca	aag	cag	acc	ggg	gtc	aaa	cgc	aag	acc	cag	aag	ccc	993
Gln	Lys	Asn	Ser	Lys	Gln	Thr	Gly	Val	Lys	Arg	Lys	Thr	Gln	Lys	Pro	
	180						185					190				
gtg	ttt	gag	gag	cgc	tac	acc	ttc	gag	atc	ccc	ttc	ctg	gag	gcc	cag	1041
Val	Phe	Glu	Glu	Arg	Tyr	Thr	Phe	Glu	Ile	Pro	Phe	Leu	Glu	Ala	Gln	
	195					200				205						
agg	agg	acc	ctg	ctc	ctg	acc	gtg	gtg	gat	ttt	gat	aag	ttc	tcc	cgc	1089
Arg	Arg	Thr	Leu	Leu	Leu	Thr	Val	Val	Asp	Phe	Asp	Lys	Phe	Ser	Arg	
210					215					220					225	
cac	tgt	gtc	att	ggg	aaa	gtt	tct	gtg	cct	ttg	tgt	gaa	gtt	gac	ctg	1137
His	Cys	Val	Ile	Gly	Lys	Val	Ser	Val	Pro	Leu	Cys	Glu	Val	Asp	Leu	
				230					235					240		
gtc	aag	ggc	ggg	cac	tgg	tgg	aag	gcg	ctg	att	ccc	agt	tct	cag	aat	1185
Val	Lys	Gly	Gly	His	Trp	Trp	Lys	Ala	Leu	Ile	Pro	Ser	Ser	Gln	Asn	
			245					250					255			
gaa	gtg	gag	ctg	ggg	gag	ctg	ctt	ctg	tca	ctg	aat	tat	ctc	cca	agt	1233
Glu	Val	Glu	Leu	Gly	Glu	Leu	Leu	Leu	Ser	Leu	Asn	Tyr	Leu	Pro	Ser	
	260					265						270				
gct	ggc	aga	ctg	aat	gtt	gat	gtc	att	cga	gcc	aag	caa	ctt	ctt	cag	1281
Ala	Gly	Arg	Leu	Asn	Val	Asp	Val	Ile	Arg	Ala	Lys	Gln	Leu	Leu	Gln	
	275				280						285					
aca	gat	gtg	agc	caa	ggt	tca	gac	ccc	ttt	gtg	aaa	atc	cag	ctg	gtg	1329
Thr	Asp	Val	Ser	Gln	Gly	Ser	Asp	Pro	Phe	Val	Lys	Ile	Gln	Leu	Val	
290					295					300					305	
cat	gga	ctc	aaa	ctt	gtg	aaa	acc	aag	aag	acg	tcc	ttc	tta	agg	ggc	1377
His	Gly	Leu	Lys	Leu	Val	Lys	Thr	Lys	Lys	Thr	Ser	Phe	Leu	Arg	Gly	
				310					315					320		
aca	att	gat	cct	ttc	tac	aat	gaa	tcc	ttc	agc	ttc	aaa	gtt	ccc	caa	1425
Thr	Ile	Asp	Pro	Phe	Tyr	Asn	Glu	Ser	Phe	Ser	Phe	Lys	Val	Pro	Gln	
			325					330					335			
gaa	gaa	ctg	gaa	aat	gcc	agc	cta	gtg	ttt	aca	gtt	ttc	ggc	cac	aac	1473
Glu	Glu	Leu	Glu	Asn	Ala	Ser	Leu	Val	Phe	Thr	Val	Phe	Gly	His	Asn	
	340					345						350				
atg	aag	agc	agc	aat	gac	ttc	atc	ggg	agg	atc	gtc	att	ggc	cag	tac	1521
Met	Lys	Ser	Ser	Asn	Asp	Phe	Ile	Gly	Arg	Ile	Val	Ile	Gly	Gln	Tyr	
	355				360					365						
tct	tca	ggc	ccc	tct	gag	acc	aac	cac	tgg	agg	cgc	atg	ctc	aac	acg	1569
Ser	Ser	Gly	Pro	Ser	Glu	Thr	Asn	His	Trp	Arg	Arg	Met	Leu	Asn	Thr	
370					375					380					385	
cac	cgc	aca	gcc	gtg	gag	cag	tgg	cat	agc	ctg	agg	tcc	cga	gct	gag	1617
His	Arg	Thr	Ala	Val	Glu	Gln	Trp	His	Ser	Leu	Arg	Ser	Arg	Ala	Glu	
			390					395					400			
tgt	gac	cgc	gtg	tct	cct	gcc	tcc	ctg	gag	gtg	acc	tgagg	gctgc			1663
Cys	Asp	Arg	Val	Ser	Pro	Ala	Ser	Leu	Glu	Val	Thr					
			405					410								

355 360 365
Tyr Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn
370 375 380
Thr His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala
385 390 395 400
Glu Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr
405 410

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<222> 76..339

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<222> 340..941

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<222> 903..908

<220>
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<222> 926..941

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ccgaccccct gcacc atg gac ccc gct cgc ccc ctg ggg ctg tcg att ctg 111
Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu
-20 -15
ctg ctt ttc ctg acg gag gct gca ctg ggc gat gct gct cag gag cca 159
Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro
-10 -5 1
aca gga aat aac gcg gag atc tgt ctc ctg ccc cta gac tac gga ccc 207
Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro
5 10 15 20
tgc cgg gcc cta ctt ctc cgt tac tac tac gac agg tac acg cag agc 255
Cys Arg Ala Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser
25 30 35
tgc cgc cag ttc ctg tac ggg ggc tgc gag ggc aac gcc aac aat ttc 303
Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe
40 45 50
tac acc tgg gag gct tgc gac gat ctt gct gga gga tagaaaaagt 349
Tyr Thr Trp Glu Ala Cys Asp Asp Leu Ala Gly Gly
55 60
tcccaaagtt tgccggctgc aagtgagtgt ggacgaccag tgtgaggggt ccacagaaaa 409

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gtatttcttt aatctaagtt ccatgacatg tgaaaaattc ttttccggtg ggtgtcaccg 469
gaaccggatt gagaacaggt ttccagatga agctacttgt atgggcttct gcgcaccaaa 529
gaaaattcca tcatttttgct acagtccaaa agatggggac tgtgctctgc caatgtgact 589
cgctattatt ttaatccaag atacagaacc tgtgatgctt tcacctatac tggctgtgga 649
gggaatgaca ataactttgt tagcagggag gattgcaaac gtgcatgtgc aaaagctttg 709
aaaaagaaaa agaagatgcc aaagcttcgc tttgccagta gaatccggaa aattcggaag 769
aagcaatttt aaacattctt aatatgtcat cttgtttgtc tttatggctt atttgccttt 829
atggttgtat ctgaagaata atatgacagc atgaggaaac aaatcattgg tgatttattc 889
accagttttt attaatacaa gtcacttttt aaaaataaaa aaaaaaaaaa aa 941
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<211> 88
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<213> Homo sapiens
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<221> SIGNAL
<222> 1..24
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Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
          -5          1          5
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
    10          15          20
Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
25          30          35          40
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
          45          50          55
Ala Cys Asp Asp Leu Ala Gly Gly
          60
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<212> DNA
<213> Homo sapiens
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<222> 1..20
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<220>
<221> CDS
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<221> 3'UTR
<222> 1119..1894
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<222> 1858..1863
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<220>

<221> polyA_site

<222> 1879..1894

<400> 27

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      Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala
                    -20                    -15
ctg gct ctt ctt tca gcg ttt tcg gcc acc cag gca cgg aaa ggc ttc 101
Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe
      -10      -5      1
tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag 149
Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln
5      10      15      20
atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc 197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser
      25      30      35
ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg 245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg
      40      45      50
cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac ccg gtg ggc 293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly
      55      60      65
atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc 341
Met Arg Arg Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu
      70      75      80
cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag 389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu
85      90      95      100
ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag 437
Gly Leu Arg Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln
      105      110      115
gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg 485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly
      120      125      130
gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct 533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala
      135      140      145
ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc 581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe
      150      155      160
aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg 629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly
165      170      175      180
cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc 677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala
      185      190      195
agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc 725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu
      200      205      210
acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac 773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp
      215      220      225
cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag 821

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Gln Leu Arg Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu
 230 235 240
 gaa ggg gcc ggc ccg gac ccc cag atg ctc tcc gag gag gtg cgc cag 869
 Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln
 245 250 255 260
 cga ctt cag gct ttc cgc cag gac acc tac ctg cag ata gct gcc ttc 917
 Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe
 265 270 275
 act cgc gcc atc gac cag gag act gag gag gtc cag cag cag ctg gcg 965
 Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala
 280 285 290
 cca cct cca cca ggc cac agt gcc ttc gcc cca gag ttt caa caa aca 1013
 Pro Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr
 295 300 305
 gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg 1061
 Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu
 310 315 320
 tgg gaa gac atc act cac agc ctt cat gac cag ggc cac agc cat ctg 1109
 Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu
 325 330 335 340
 ggg gac ccc tgaggatcta cctgcccagg cccattccca gcttcttgtc 1158
 Gly Asp Pro
 tgggggagcct tggtctctgag cctctagcat gggttcagtcc ttgaaagtgg cctgttgggt 1218
 ggagggtgga aggtcctgtg caggacaggg aggccaccaa aggggctgct gtctcctgca 1278
 tatccagcct cctgcgactc cccaatctgg atgcattaca ttcaccaggc tttgcaaacc 1338
 cagcctccca gtgctcattt gggaatgctc atgagttact ccattcaagg gtgagggagt 1398
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 ggaagcctgt gccactacat cctggagttt ggctctagtc acttctggct gcctggtggc 1518
 cactgctaca gctggtccac agagaggagc acttgtctcc ccagggctgc catggcagct 1578
 atcaggggaa tagaaggag aaagagaata tcatggggag aacatgtgat ggtgtgtgaa 1638
 tatccctgct ggctctgatg ctggtgggta cgaaaggtgt gggctgtgat aggagagggc 1698
 agagcccatg tttcctgaca tagctctaca cctaaataag ggactgaacc ctcccaactg 1758
 tgggagctcc ttaaaccctc tggggagcat actgtgtgct ctcccatct ccagcccctc 1818
 cctctgggtt cccaagttga agcctagact tctggctcaa atgaaataga tgtttatgat 1878
 aaaaaaaaaa aaaaaa 1894

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..23

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 Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser
 -5 1 5
 Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
 10 15 20 25
 Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
 30 35 40

Asn	Asn	Met	Asn	Lys	Phe	Leu	Glu	Lys	Leu	Arg	Pro	Leu	Ser	Gly	Ser
			45					50					55		
Glu	Ala	Pro	Arg	Leu	Pro	Gln	Asp	Pro	Val	Gly	Met	Arg	Arg	Gln	Leu
		60					65					70			
Gln	Glu	Glu	Leu	Glu	Glu	Val	Lys	Ala	Arg	Leu	Gln	Pro	Tyr	Met	Ala
		75				80					85				
Glu	Ala	His	Glu	Leu	Val	Gly	Trp	Asn	Leu	Glu	Gly	Leu	Arg	Gln	Gln
90					95					100					105
Leu	Lys	Pro	Tyr	Thr	Met	Asp	Leu	Met	Glu	Gln	Val	Ala	Leu	Arg	Val
				110						115				120	
Gln	Glu	Leu	Gln	Glu	Gln	Leu	Arg	Val	Val	Gly	Glu	Asp	Thr	Lys	Ala
			125					130					135		
Gln	Leu	Leu	Gly	Gly	Val	Asp	Glu	Ala	Trp	Ala	Leu	Leu	Gln	Gly	Leu
		140					145					150			
Gln	Ser	Arg	Val	Val	His	His	Thr	Gly	Arg	Phe	Lys	Glu	Leu	Phe	His
		155				160					165				
Pro	Tyr	Ala	Glu	Ser	Leu	Val	Ser	Gly	Ile	Gly	Arg	His	Val	Gln	Glu
170					175					180					185
Leu	His	Arg	Ser	Val	Ala	Pro	His	Ala	Pro	Ala	Ser	Pro	Ala	Arg	Leu
				190						195				200	
Ser	Arg	Cys	Val	Gln	Val	Leu	Ser	Arg	Lys	Leu	Thr	Leu	Lys	Ala	Lys
		205						210					215		
Ala	Leu	His	Ala	Arg	Ile	Gln	Gln	Asn	Leu	Asp	Gln	Leu	Arg	Glu	Glu
		220				225						230			
Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu	Glu	Gly	Ala	Gly	Pro
		235				240					245				
Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln	Arg	Leu	Gln	Ala	Phe
250					255					260					265
Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	Thr	Arg	Ala	Ile	Asp
				270						275				280	
Gln	Glu	Thr	Glu	Glu	Val	Gln	Gln	Gln	Leu	Ala	Pro	Pro	Pro	Pro	Gly
			285					290					295		
His	Ser	Ala	Phe	Ala	Pro	Glu	Phe	Gln	Gln	Thr	Asp	Ser	Gly	Lys	Val
		300					305					310			
Leu	Ser	Lys	Leu	Gln	Ala	Arg	Leu	Asp	Asp	Leu	Trp	Glu	Asp	Ile	Thr
		315				320					325				
His	Ser	Leu	His	Asp	Gln	Gly	His	Ser	His	Leu	Gly	Asp	Pro		
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Arg Val Ser Asp Leu	Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys			
20	25	30		
agt gga ctg aag cac	gag ctc gtc acc agg gcc ctc cag ctg gtg cag			144
Ser Gly Leu Lys His	Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln			
35	40	45		
ttt gac tgt acc cct	gag ctg ttc aag aag atc aag gag ctg tac gag			192
Phe Asp Cys Thr Pro	Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu			
50	55	60		
acc cgc tac gcc aag	aag aac tcg gag cct gcc cca cag ccg cac cgg			240
Thr Arg Tyr Ala Lys	Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg			
65	70	75		
ccc ctg gac ccc ctg	acc atg cac tcc acc tac gac cgg gcc ggc gct			288
Pro Leu Asp Pro Leu	Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala			
80	85	90	95	
gtg ccc agg act ccg	ctg gca ggc ccc aat att gac tac ccc gtg ctc			336
Val Pro Arg Thr Pro	Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu			
100	105	110		
tac gga aag tac tta	aac gga ctg gga cgg ttg ccc gcc aag acc ctc			384
Tyr Gly Lys Tyr Leu	Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu			
115	120	125		
aag cca gaa gtc cgc	ctg gtg aag ctg ccg ttc ttt aat atg ctg gac			432
Lys Pro Glu Val Arg	Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp			
130	135	140		
gag ctg ctg aag ccc	acc gaa tta gtc cca cag aac aac gag aag ctt			480
Glu Leu Leu Lys Pro	Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu			
145	150	155		
cag gag agc ccg tgc	atc ttc gca ttg acg cca aga cag gtg gag ttg			528
Gln Glu Ser Pro Cys	Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu			
160	165	170	175	
atc cgg aac tcc agg	gaa ctg cag ccc gga gtt aaa gcc gtg cag gtc			576
Ile Arg Asn Ser Arg	Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val			
180	185	190		
gtc ctg aga atc tgt	tac tca gac acc agc tgc cct cag gag gac cag			624
Val Leu Arg Ile Cys	Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln			
195	200	205		
tac ccg ccc aac atc	gct gtg aag gtc aac cac agc tac tgc tcc gtc			672
Tyr Pro Pro Asn Ile	Ala Val Lys Val Asn His Ser Tyr Cys Ser Val			
210	215	220		
ccg ggc tac tac ccc	tcc aat aag ccc ggg gtg gag ccc aag agg ccg			720
Pro Gly Tyr Tyr Pro	Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro			
225	230	235		
tgc cgc ccc atc aac	ctc acc cac ctc atg tac ctt tcc tcg gcc acc			768
Cys Arg Pro Ile Asn	Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr			
240	245	250	255	
aac cgc atc act gtc	acc tgg ggg aac tac ggc aag agc tac tcg gtg			816
Asn Arg Ile Thr Val	Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val			
260	265	270		
gcc ctg tac ctg gtg	cgg cag ctg acc tca tcg gag ctg ctg cag agg			864
Ala Leu Tyr Leu Val	Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg			
275	280	285		
ctg aag acc att ggg	gta aag cac ccg gag ctg tgc aag gca ctg gtc			912
Leu Lys Thr Ile Gly	Val Lys His Pro Glu Leu Cys Lys Ala Leu Val			

	290						295				300							
aag	gag	aag	ctg	cgc	ctt	gat	cct	gac	agc	gag	atc	gcc	acc	acc	ggc	960		
Lys	Glu	Lys	Leu	Arg	Leu	Asp	Pro	Asp	Ser	Glu	Ile	Ala	Thr	Thr	Gly			
	305						310				315							
gtg	cgg	gtg	tcc	ctc	atc	tgt	ccg	ctg	gtg	aag	atg	cgg	ctc	tcc	gtg	1008		
Val	Arg	Val	Ser	Leu	Ile	Cys	Pro	Leu	Val	Lys	Met	Arg	Leu	Ser	Val			
320					325					330					335			
ccc	tgc	cgg	gca	gag	acc	tgc	gcc	cac	ctg	cag	tgc	ttc	gac	gcc	gtc	1056		
Pro	Cys	Arg	Ala	Glu	Thr	Cys	Ala	His	Leu	Gln	Cys	Phe	Asp	Ala	Val			
				340					345					350				
ttc	tac	ctg	cag	atg	aac	gag	aag	aag	ccc	acc	tgg	atg	tgc	ccc	gtg	1104		
Phe	Tyr	Leu	Gln	Met	Asn	Glu	Lys	Lys	Pro	Thr	Trp	Met	Cys	Pro	Val			
			355					360					365					
tgc	gac	aag	cca	gcc	ccc	tac	gac	cag	ctc	atc	atc	gac	ggg	ctc	ctc	1152		
Cys	Asp	Lys	Pro	Ala	Pro	Tyr	Asp	Gln	Leu	Ile	Ile	Asp	Gly	Leu	Leu			
		370					375					380						
tcg	aag	atc	ctg	agc	gag	tgt	gag	gac	gcc	gac	gag	atc	gag	tac	ctg	1200		
Ser	Lys	Ile	Leu	Ser	Glu	Cys	Glu	Asp	Ala	Asp	Glu	Ile	Glu	Tyr	Leu			
	385					390						395						
gtg	gac	ggc	tcg	tgg	tgc	ccg	atc	cgc	gcc	gaa	aag	gag	ctc	agc	tgc	1248		
Val	Asp	Gly	Ser	Trp	Cys	Pro	Ile	Arg	Ala	Glu	Lys	Glu	Leu	Ser	Cys			
400					405					410					415			
agc	ccg	cag	ggc	gcc	atc	ctc	gtg	ctg	ggc	ccc	tcg	gac	gcc	aat	ggg	1296		
Ser	Pro	Gln	Gly	Ala	Ile	Leu	Val	Leu	Gly	Pro	Ser	Asp	Ala	Asn	Gly			
			420						425					430				
ctc	ctg	ccc	gcc	ccc	agc	gtc	aac	ggg	agc	ggc	gcc	ctg	ggc	agc	acg	1344		
Leu	Leu	Pro	Ala	Pro	Ser	Val	Asn	Gly	Ser	Gly	Ala	Leu	Gly	Ser	Thr			
			435					440					445					
ggc	ggc	ggc	ggc	ccg	gtg	ggc	agc	atg	gag	aat	ggg	aag	ccg	ggc	gcc	1392		
Gly	Gly	Gly	Gly	Pro	Val	Gly	Ser	Met	Glu	Asn	Gly	Lys	Pro	Gly	Ala			
		450				455						460						
gat	gtg	gtg	gac	ctc	acg	ctg	gac	agc	tca	tcg	tcc	tcg	gag	gat	gag	1440		
Asp	Val	Val	Asp	Leu	Thr	Leu	Asp	Ser	Ser	Ser	Ser	Ser	Glu	Asp	Glu			
	465					470						475						
gag	gag	gag	gaa	gag	gag	gag	gaa	gac	gag	gac	gaa	gag	ggg	ccc	cgg	1488		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Gly	Pro	Arg			
480					485					490					495			
ccc	aag	cgc	cgc	tgc	ccc	ttc	cag	aag	ggc	ctg	gtg	ccg	gcc	tgc		1533		
Pro	Lys	Arg	Arg	Cys	Pro	Phe	Gln	Lys	Gly	Leu	Val	Pro	Ala	Cys				
			500					505					510					
tgacccccggc	cgcacacttg	acttttcctgg	tgctcacc															

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<210> 32
<211> 510
<212> PRT
<213> Homo sapiens
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<400> 32
Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg
1          5          10          15
Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
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450	455	460
Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu Glu		
465	470	475
Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg Pro		480
	485	490
Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys		495
	500	505
		510

<210> 33
 <211> 877
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..10

<220>
 <221> CDS
 <222> 11..802

<220>
 <221> 3'UTR
 <222> 803..877

<220>
 <221> polyA_signal
 <222> 836..841

<220>
 <221> polyA_site
 <222> 862..877

<400> 33	
atctgccacg atg ttg ctg ctc agc ctg acc cta agc ctg gtt ctc ctc	49
Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu	
-15	-10
ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc	97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser	
-5	1
ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg	145
Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp	
15	20
ccc tgg cag gtg tcc ctg cag gac agc agc gac ttc cac ttc tgc ggt	193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly	
30	35
ggc tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat	241
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn	
45	50
gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca	289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser	
60	65
tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca	337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr	
70	75

[illegible]

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<210> 34
<211> 264
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> 1..18
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<400> 34
Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser
      -15                      -10                      -5
Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln
      1                      5                      10
Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
15                      20                      25                      30
Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly Gly Ser Leu
      35                      40                      45
Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
      50                      55                      60
Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala

```

```
<210> 35
<211> 1728
<212> DNA
<213> Homo sapiens
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<220>
<221> 5'UTR
<222> 1..37

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<220>  
<221> CDS  
<222> 38..1378
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<220>
<221> 3'UTR
<222> 1379..1728
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<220>  
<221> polyA_site  
<222> 1713..1728
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<400> 35
atcatctgca cagctggggc ccctgggagg agacgcc atg atc ccc acc ttc acg      55
                                     Met Ile Pro Thr Phe Thr
                                     -20
gct ctg ctc tgc ctc ggg ctg agt ctg ggc ccc agg acc cac atg cag      103
Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Met Gln
      -15                      -10                      -5
gca ggg ccc ctc ccc aaa ccc acc ctc tgg gct gag cca ggc tct gtg      151
Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val

```

1				5				10				15				
atc	agc	tgg	ggg	aac	tct	gtg	acc	atc	tgg	tgt	cag	ggg	acc	ctg	gag	199
Ile	Ser	Trp	Gly	Asn	Ser	Val	Thr	Ile	Trp	Cys	Gln	Gly	Thr	Leu	Glu	
20				25				30								
gct	cgg	gag	tac	cgt	ctg	gat	aaa	gag	gaa	agc	cca	gca	ccc	tgg	gac	247
Ala	Arg	Glu	Tyr	Arg	Leu	Asp	Lys	Glu	Glu	Ser	Pro	Ala	Pro	Trp	Asp	
35				40				45								
aga	cag	aac	cca	ctg	gag	ccc	aag	aac	aag	gcc	aga	ttc	tcc	atc	cca	295
Arg	Gln	Asn	Pro	Leu	Glu	Pro	Lys	Asn	Lys	Ala	Arg	Phe	Ser	Ile	Pro	
50				55				60								
tcc	atg	aca	gag	gac	tat	gca	ggg	aga	tac	cgc	tgt	tac	tat	cgc	agc	343
Ser	Met	Thr	Glu	Asp	Tyr	Ala	Gly	Arg	Tyr	Arg	Cys	Tyr	Tyr	Arg	Ser	
65				70				75								
cct	gta	ggc	tgg	tca	cag	ccc	agt	gac	ccc	ctg	gag	ctg	gtg	atg	aca	391
Pro	Val	Gly	Trp	Ser	Gln	Pro	Ser	Asp	Pro	Leu	Glu	Leu	Val	Met	Thr	
80				85				90				95				
gga	gcc	tac	agt	aaa	ccc	acc	ctt	tca	gcc	ctg	ccg	agt	cct	ctt	gtg	439
Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	Ala	Leu	Pro	Ser	Pro	Leu	Val	
100				105				110								
acc	tca	gaa	aag	agc	gtg	acc	ctg	ctg	tgt	cag	tca	cgg	agc	cca	atg	487
Thr	Ser	Glu	Lys	Ser	Val	Thr	Leu	Leu	Cys	Gln	Ser	Arg	Ser	Pro	Met	
115				120				125								
gac	act	ttc	ctt	ctg	atc	aag	gag	cgg	gca	gcc	cat	ccc	cta	ctg	cat	535
Asp	Thr	Phe	Leu	Leu	Ile	Lys	Glu	Arg	Ala	Ala	His	Pro	Leu	Leu	His	
130				135				140								
ctg	aga	tca	gag	cac	gga	gct	cag	cag	cac	cag	gct	gaa	ttc	ccc	atg	583
Leu	Arg	Ser	Glu	His	Gly	Ala	Gln	Gln	His	Gln	Ala	Glu	Phe	Pro	Met	
145				150				155								
agt	cct	gtg	acc	tca	gtg	cac	ggg	ggg	acc	tac	agg	tgc	ttc	agc	tca	631
Ser	Pro	Val	Thr	Ser	Val	His	Gly	Gly	Thr	Tyr	Arg	Cys	Phe	Ser	Ser	
160				165				170				175				
cac	ggc	ttc	tcc	cac	tac	ctg	ctg	tca	cac	ccc	agt	gac	ccc	ctg	gag	679
His	Gly	Phe	Ser	His	Tyr	Leu	Leu	Ser	His	Pro	Ser	Asp	Pro	Leu	Glu	
180				185				190								
ctc	ata	gtc	tca	gga	tcc	ttg	gag	gat	ccc	agg	ccc	tca	ccc	aca	agg	727
Leu	Ile	Val	Ser	Gly	Ser	Leu	Glu	Asp	Pro	Arg	Pro	Ser	Pro	Thr	Arg	
195				200				205								
tcc	gtc	tca	aca	gct	gca	ggc	cct	gag	gac	cag	ccc	ctc	atg	cct	aca	775
Ser	Val	Ser	Thr	Ala	Ala	Gly	Pro	Glu	Asp	Gln	Pro	Leu	Met	Pro	Thr	
210				215				220								
ggg	tca	gtc	ccc	cac	agt	ggt	ctg	aga	agg	cac	tgg	gag	gta	ctg	atc	823
Gly	Ser	Val	Pro	His	Ser	Gly	Leu	Arg	Arg	His	Trp	Glu	Val	Leu	Ile	
225				230				235								
ggg	gtc	ttg	gtg	gtc	tcc	atc	ctg	ctt	ctc	tcc	ctc	ctc	ctc	ttc	ctc	871
Gly	Val	Leu	Val	Val	Ser	Ile	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Phe	Leu	
240				245				250				255				
ctc	ctc	caa	cac	tgg	cgt	cag	gga	aaa	cac	agg	aca	ttg	gcc	cag	aga	919
Leu	Leu	Gln	His	Trp	Arg	Gln	Gly	Lys	His	Arg	Thr	Leu	Ala	Gln	Arg	
260				265				270								
cag	gct	gat	ttc	caa	cgt	cct	cca	ggg	gct	gcc	gag	cca	gag	ccc	aag	967
Gln	Ala	Asp	Phe	Gln	Arg	Pro	Pro	Gly	Ala	Ala	Glu	Pro	Glu	Pro	Lys	
275				280				285								
gac	ggg	ggc	cta	cag	agg	agg	tcc	agc	cca	gct	gct	gac	gtc	cag	gga	1015
Asp	Gly	Gly	Leu	Gln	Arg	Arg	Ser	Ser	Pro	Ala	Ala	Asp	Val	Gln	Gly	

			290			295						300						
gaa	aac	ttc	tgt	gct	gcc	gtg	aag	gac	aca	cag	cct	gag	gac	ggg	gtg		1063	
Glu	Asn	Phe	Cys	Ala	Ala	Val	Lys	Asp	Thr	Gln	Pro	Glu	Asp	Gly	Val			
			305			310						315						
gaa	atg	gac	act	cgg	agc	cca	cac	gat	gaa	gac	ccc	cag	gca	gtg	acg		1111	
Glu	Met	Asp	Thr	Arg	Ser	Pro	His	Asp	Glu	Asp	Pro	Gln	Ala	Val	Thr			
320						325						330			335			
tat	gcc	aag	gtg	aaa	cac	tcc	aga	cct	agg	aga	gaa	atg	gcc	tct	cct		1159	
Tyr	Ala	Lys	Val	Lys	His	Ser	Arg	Pro	Arg	Arg	Glu	Met	Ala	Ser	Pro			
			340						345						350			
ccc	tcc	cca	ctg	tct	ggg	gaa	ttc	ctg	gac	aca	aag	gac	aga	cag	gca		1207	
Pro	Ser	Pro	Leu	Ser	Gly	Glu	Phe	Leu	Asp	Thr	Lys	Asp	Arg	Gln	Ala			
			355			360						365						
gaa	gag	gac	aga	cag	atg	gac	act	gag	gct	gct	gca	tct	gaa	gcc	ccc		1255	
Glu	Glu	Asp	Arg	Gln	Met	Asp	Thr	Glu	Ala	Ala	Ala	Ser	Glu	Ala	Pro			
			370			375						380						
cag	gat	gtg	acc	tac	gcc	cag	ctg	cac	agc	ttt	acc	ctc	aga	cag	aag		1303	
Gln	Asp	Val	Thr	Tyr	Ala	Gln	Leu	His	Ser	Phe	Thr	Leu	Arg	Gln	Lys			
385						390						395						
gca	act	gag	cct	cct	cca	tcc	cag	gaa	ggg	gcc	tct	cca	gct	gag	ccc		1351	
Ala	Thr	Glu	Pro	Pro	Pro	Ser	Gln	Glu	Gly	Ala	Ser	Pro	Ala	Glu	Pro			
400			405						410						415			
agt	gtc	tat	gcc	act	ctg	gcc	atc	cac	taatccaggg gggacccaga								1398	
Ser	Val	Tyr	Ala	Thr	Leu	Ala	Ile	His										
			420															
ccccacaagc			catggagact			caggacccca			gaaggcatgg			aagctgcctc			cagtagacat			1458
cactgaaccc			cagccagccc			agaccctga			cacagaccac			tagaagattc			cggaacggtt			1518
gggagtcacc			tgattctgca			aagataaata			atatccctgc			attatcaaaa			taaagtagca			1578
gacctctcaa			ttcacaatga			gttaactgat			aaaacaaaac			agaagtcaga			caatgtttta			1638
aattgaatga			tcatgtaaat			attacacatc			aaaccaatga			catgggaaaa			tgggagcttc			1698
taatgaggac			aaacaaaaaa			aaaaaaaaaa												1728

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<210> 36
<211> 447
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> 1..23
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<400> 36
Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
      -20                      -15                      -10
Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
      -5                      1                      5
Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp
10                      15                      20                      25
Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
      30                      35                      40
Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
      45                      50                      55
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
      60                      65                      70

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Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
 75      80      85
Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala
 90      95     100     105
Leu Pro Ser Pro Leu Val Thr Ser Glu Lys Ser Val Thr Leu Leu Cys
      110     115     120
Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
      125     130     135
Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His
      140     145     150
Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
      155     160     165
Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
      170     175     180     185
Pro Ser Asp Pro Leu Glu Leu Ile Val Ser Gly Ser Leu Glu Asp Pro
      190     195     200
Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
      205     210     215
Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
      220     225     230
His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
      235     240     245
Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His
      250     255     260     265
Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
      270     275     280
Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro
      285     290     295
Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asp Thr
      300     305     310
Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu
      315     320     325
Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro Arg
      330     335     340     345
Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp
      350     355     360
Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala
      365     370     375
Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser
      380     385     390
Phe Thr Leu Arg Gln Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly
      395     400     405
Ala Ser Pro Ala Glu Pro Ser Val Tyr Ala Thr Leu Ala Ile His
      410     415     420

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<210> 37
 <211> 1757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..329

<220>
 <221> CDS
 <222> 330..1478

<220>
 <221> 3'UTR
 <222> 1479..1757

<220>
 <221> polyA_signal
 <222> 1722..1727

<220>
 <221> polyA_site
 <222> 1742..1757

<400> 37
 atttagttga agctgcaggg gagtgagggg gaggaggata ggaagcagga aagcgggaga 60
 gctcgagggg caaggggggct cgggtgtgtt acaccaggca cgggctacga gcgtccatcc 120
 cggcccctgg cttgcgctcc cgaagaggag agcaaggctg ttctgggata cggccgtcgt 180
 gcggcaagag gcttgtctgt ccgggttgcc ggaaccagga gaaccagag ggaaaccgag 240
 gcaaaggagc ggcgcgtttt actagagaga gcgcgagcgg aagaggcgag agcaggagcg 300
 cgcgagggag catcgagcgc agcggagac atg agg acc tac tgg ctg cac agc 353
 Met Arg Thr Tyr Trp Leu His Ser
 -20
 gtc tgg gtg ctg ggc ttt ttc ctg tcc ctc ttc tca ttg caa gga ctg 401
 Val Trp Val Leu Gly Phe Phe Leu Ser Leu Phe Ser Leu Gln Gly Leu
 -15 -10 -5 1
 cct gtt cgc agc gtg gat ttt aac cga ggc acg gac aac atc acc gtg 449
 Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val
 5 10 15
 agg cag ggg gac aca gcc atc ctc agg tgc gtt gta gaa gac aag aac 497
 Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn
 20 25 30
 tca aag gtg gcc tgg ttg aac cgt tct ggc atc att ttt gct gga cat 545
 Ser Lys Val Ala Trp Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His
 35 40 45
 gac aag tgg tct ctg gac cca cgg gtt gag ctg gag aaa cgc cat tct 593
 Asp Lys Trp Ser Leu Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser
 50 55 60 65
 ctg gaa tac agc ctc cga atc cag aag gtg gat gtc tat gat gag ggt 641
 Leu Glu Tyr Ser Leu Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly
 70 75 80
 tcc tac act tgc tca gtt cag aca cag cat gag ccc aag acc tcc caa 689
 Ser Tyr Thr Cys Ser Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln
 85 90 95
 gtt tac ttg atc gta caa gtc cca cca aag atc tcc aat atc tcc tcg 737
 Val Tyr Leu Ile Val Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser
 100 105 110
 gat gtc act gtg aat gag ggc agc aac gtg act ctg gtc tgc atg gcc 785
 Asp Val Thr Val Asn Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala
 115 120 125
 aat ggc cgt cct gaa cct gtt atc acc tgg aga cac ctt aca cca act 833
 Asn Gly Arg Pro Glu Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr

130	135	140	145	
gga agg gaa ttt gaa gga gaa gaa gaa tat ctg gag atc ctt ggc atc				881
Gly Arg Glu Phe Glu Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile				
150	155	160		
acc agg gag cag tca ggc aaa tat gag tgc aaa gct gcc aac gag gtc				929
Thr Arg Glu Gln Ser Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val				
165	170	175		
tcc tcg gcg gat gtc aaa caa gtc aag gtc act gtg aac tat cct ccc				977
Ser Ser Ala Asp Val Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro				
180	185	190		
act atc aca gaa tcc aag agc aat gaa gcc acc aca gga cga caa gct				1025
Thr Ile Thr Glu Ser Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala				
195	200	205		
tca ctc aaa tgt gag gcc tcg gca gtg cct gca cct gac ttt gag tgg				1073
Ser Leu Lys Cys Glu Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp				
210	215	220		
tac cgg gat gac act agg ata aat agt gcc aat ggc ctt gag att aag				1121
Tyr Arg Asp Asp Thr Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys				
230	235	240		
agc acg gag ggc cag tct tcc ctg acg gtg acc aac gtc act gag gag				1169
Ser Thr Glu Gly Gln Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu				
245	250	255		
cac tac ggc aac tac acc tgt gtg gct gcc aac aag ctg ggg gtc acc				1217
His Tyr Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr				
260	265	270		
aat gcc agc cta gtc ctt ttc aaa cgt gtt tta ccc aca atc ccc cac				1265
Asn Ala Ser Leu Val Leu Phe Lys Arg Val Leu Pro Thr Ile Pro His				
275	280	285		
ccc att caa gaa att ggt acc acc gtg cac ttc aag caa aaa ggc atc				1313
Pro Ile Gln Glu Ile Gly Thr Thr Val His Phe Lys Gln Lys Gly Ile				
290	295	300		
ttc ctc tct gag tct cag agg ggt gag aca acc aag atc act ctc aac				1361
Phe Leu Ser Glu Ser Gln Arg Gly Glu Thr Thr Lys Ile Thr Leu Asn				
310	315	320		
tgt gga aat cta ttc ttg cgg aac tta cat ccc acc agt gat caa gag				1409
Cys Gly Asn Leu Phe Leu Arg Asn Leu His Pro Thr Ser Asp Gln Glu				
325	330	335		
cca cag aga tta tgg aca ctt tgt tgc tta ctc cca aga aag ggc cag				1457
Pro Gln Arg Leu Trp Thr Leu Cys Cys Leu Leu Pro Arg Lys Gly Gln				
340	345	350		
cac cgt att tat ggc cag tgc tagaagggtcc tcaactgaagg caacagggaa				1508
His Arg Ile Tyr Gly Gln Cys				
355	360			
gaggcagcca tgaatatata cttggaaaca ggatcatttg aggccttcaa gaaggcataa				1568
aatattgtcc ctttcagcct ttcttttctt ctcaatgccca cgattaccaa ttatgtttta				1628
atcttaagtg gctagtgtta tatgtgatac attatgcctt tgatatgtgg ttgaaaaaat				1688
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 <213> Homo sapiens


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<210> 39
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<212> DNA
<213> Homo sapiens
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Ser Leu Gln Lys His Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu	
140 145 150 155	
tcc aat aag atc cca gag ctg gac atg act gag gtg gtg gcc ccc ttc	593
Ser Asn Lys Ile Pro Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe	
160 165 170	
atg gcc aac atc cct ctc ctc ctc tac cct cag gac ggc ccc cgc agc	641
Met Ala Asn Ile Pro Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser	
175 180 185	
aag ccc cag cca aag gat aat ggg gac gtt tgc cag gac tgc att cag	689
Lys Pro Gln Pro Lys Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln	
190 195 200	
atg gtg act gac atc cag act gct gta cgg acc aac tcc acc ttt gtc	737
Met Val Thr Asp Ile Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val	
205 210 215	
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Gln Ala Leu Val Glu His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro	
220 225 230 235	
ggc atg gcc gac ata tgc aag aac tat atc agc cag tat tct gaa att	833
Gly Met Ala Asp Ile Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile	
240 245 250	
gct atc cag atg atg atg cac atg cag gat cag caa ccc aag gag atc	881
Ala Ile Gln Met Met Met His Met Gln Asp Gln Gln Pro Lys Glu Ile	
255 260 265	
tgt gcg ctg gtt ggg ttc tgt gat gag gtg aaa gag atg ccc atg cag	929
Cys Ala Leu Val Gly Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln	
270 275 280	
act ctg gtc ccc gcc aaa gtg gcc tcc aag aat gtc atc cct gcc ctg	977
Thr Leu Val Pro Ala Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu	
285 290 295	
gaa ctg gtg gag ccc att aag aag cac gag gtc cca gca aag tct gat	1025
Glu Leu Val Glu Pro Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp	
300 305 310 315	
gtt tac tgt gag gtg tgt gaa ttc ctg gtg aag gag gtg acc aag ctg	1073
Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu	
320 325 330	
att gac aac aac aag act gag aaa gaa ata ctc gac gct ttt gac aaa	1121
Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys	
335 340 345	
atg tgc tcg aag ctg ccg aag tcc ctg tcg gaa gag tgc cag gag gtg	1169
Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val	
350 355 360	
gtg gac acg tac ggc agc tcc atc ctg tcc atc ctg ctg gag gag gtc	1217
Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val	
365 370 375	
agc cct gag ctg gtg tgc agc atg ctg cac ctc tgc tct ggc acg cgg	1265
Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg	
380 385 390 395	
ctg cct gca ctg acc gtt cac gtg act cag cca aag gac ggt ggc ttc	1313
Leu Pro Ala Leu Thr Val His Val Thr Gln Pro Lys Asp Gly Gly Phe	
400 405 410	
tgc gaa gtg tgc aag aag ctg gtg ggt tat ttg gat cgc aac ctg gag	1361
Cys Glu Val Cys Lys Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu	
415 420 425	

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aaa aac agc acc aag cag gag atc ctg gct gct ctt gag aaa ggc tgc 1409
Lys Asn Ser Thr Lys Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys
      430                      435                      440
agc ttc ctg cca gac cct tac cag aag cag tgt gat cag ttt gtg gca 1457
Ser Phe Leu Pro Asp Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala
      445                      450                      455
gag tac gag ccc gtg ctg atc gag atc ctg gtg gag gta tgg atc ctt 1505
Glu Tyr Glu Pro Val Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu
460                      465                      470                      475
cct tcg tgt gct tgaaaattgg agcctgcccc tcggcccata agcccttggt 1557
Pro Ser Cys Ala
gggaactgag aagtgtatat ggggcccag ctactggtgc cagaacacag agacagcagc 1617
ccagtgcaat gctgtcgagc attgcaaacg ccatgtgtgg aactaggagg aggaatattc 1677
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<210> 40
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 <212> PRT
 <213> Homo sapiens

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      20      25      30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
      35      40      45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
      50      55      60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65      70      75      80
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
      85      90      95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
      100      105      110

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Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
 115 120 125
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
 130 135 140
 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
 145 150 155 160
 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
 165 170 175
 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
 180 185 190
 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
 195 200 205
 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
 210 215 220
 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
 225 230 235 240
 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
 245 250 255
 Met His Met Gln Asp Gln Gln Pro Lys Glu Ile Cys Ala Leu Val Gly
 260 265 270
 Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala
 275 280 285
 Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro
 290 295 300
 Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val
 305 310 315 320
 Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
 325 330 335
 Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu
 340 345 350
 Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly
 355 360 365
 Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val
 370 375 380
 Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr
 385 390 395 400
 Val His Val Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys
 405 410 415
 Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys
 420 425 430
 Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp
 435 440 445
 Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val
 450 455 460
 Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu Pro Ser Cys Ala
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<211> 142
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 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
 -5 1 5 10
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe
 15 20 25
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
 30 35 40
 Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
 45 50 55
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
 60 65 70 75
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
 80 85 90
 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
 95 100 105

<210> 43
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 <222> 1232..1237

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 <222> 1255..1340

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<210> 44
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<213> Homo sapiens

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Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
          20          25          30
Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
          35          40          45
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser

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50 55 60
 Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
 65 70 75 80
 Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
 85 90 95
 Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
 100 105 110
 Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser
 115 120

<210> 45
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 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> 118..1632

<220>
 <221> 3'UTR
 <222> 1633..1999

<220>
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 <222> 1937..1942

<220>
 <221> polyA_site
 <222> 1956..1999

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 atg cgc ctc cgc cgc cta gcg ctg ttc ccg ggt gtg gcg ctg ctt ctt 165
 Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu
 -20 -15 -10
 gcc gcg gcc cgc ctc gcc gct gcc tcc gac gtg cta gaa ctc acg gac 213
 Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
 -5 1 5
 gac aac ttc gag agt cgc atc tcc gac acg ggc tct gcg ggc ctc atg 261
 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
 10 15 20
 ctc gtc gag ttc ttc gct ccc tgg tgt gga cac tgc aag aga ctt gca 309
 Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
 25 30 35 40
 cct gag tat gaa gct gca gct acc aga tta aaa gga ata gtc cca tta 357
 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
 45 50 55
 gca aag gtt gat tgc act gcc aac act aac acc tgt aat aaa tat gga 405

Ala	Lys	Val	Asp	Cys	Thr	Ala	Asn	Thr	Asn	Thr	Cys	Asn	Lys	Tyr	Gly	
			60					65					70			
gtc	agt	gga	tat	cca	acc	ctg	aag	ata	ttt	aga	gat	ggt	gaa	gaa	gca	453
Val	Ser	Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Asp	Gly	Glu	Glu	Ala	
		75					80					85				
ggt	gct	tat	gat	gga	cct	agg	act	gct	gat	gga	att	gtc	agc	cac	ttg	501
Gly	Ala	Tyr	Asp	Gly	Pro	Arg	Thr	Ala	Asp	Gly	Ile	Val	Ser	His	Leu	
	90					95					100					
aag	aag	cag	gca	gga	cca	gct	tca	gtg	cct	ctc	agg	act	gag	gaa	gaa	549
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu	
105					110				115						120	
ttt	aag	aaa	ttc	att	agt	gat	aaa	gat	gcc	tct	ata	gta	ggt	ttt	ttc	597
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe	
			125						130					135		
gat	gat	tca	ttc	agt	gag	gct	cac	tcc	gag	ttc	cta	aaa	gca	gcc	agc	645
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser	
			140					145					150			
aac	ttg	agg	gat	aac	tac	cga	ttt	gca	cat	acg	aat	gtt	gag	tct	ctg	693
Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu	
		155					160					165				
gtg	aac	gag	tat	gat	gat	aat	gga	gag	ggt	atc	atc	tta	ttt	cgt	cct	741
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro	
	170					175						180				
tca	cat	ctc	act	aac	aag	ttt	gag	gac	aag	act	gtg	gca	tat	aca	gag	789
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu	
185					190					195					200	
caa	aaa	atg	acc	agt	ggc	aaa	att	aaa	aag	ttt	atc	cag	gaa	aac	att	837
Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile	
				205					210					215		
ttt	ggt	atc	tgc	cct	cac	atg	aca	gaa	gac	aat	aaa	gat	ttg	ata	cag	885
Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln	
			220					225					230			
ggc	aag	gac	tta	ctt	att	gct	tac	tat	gat	gtg	gac	tat	gaa	aag	aac	933
Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn	
		235					240					245				
gct	aaa	ggt	tcc	aac	tac	agg	aga	aac	agg	gta	atg	atg	gtg	gca	aag	981
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys	
	250					255					260					
aaa	ttc	ctg	gat	gct	ggg	cac	aaa	ctc	aac	ttt	gct	gta	gct	agc	cgc	1029
Lys	Phe	Leu	Asp	Ala	Gly	His	Lys	Leu	Asn	Phe	Ala	Val	Ala	Ser	Arg	
265					270					275					280	
aaa	acc	ttt	agc	cat	gaa	ctt	tct	gat	ttt	ggc	ttg	gag	agc	act	gct	1077
Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala	
				285					290				295			
gga	gag	att	cct	gtt	gtt	gct	atc	aga	act	gct	aaa	gga	gag	aag	ttt	1125
Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe	
			300					305					310			
gtc	atg	cag	gag	gag	ttc	tcg	cgt	gat	ggg	aag	gct	ctg	gag	agg	ttc	1173
Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe	
		315					320					325				
ctg	cag	gat	tac	ttt	gat	ggc	aat	ctg	aag	aga	tac	ctg	aag	tct	gaa	1221
Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu	
	330					335					340					
cct	atc	cca	gag	agc	aat	gat	ggg	cct	gtg	aag	gta	gtg	gta	gca	gag	1269

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Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu
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Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
          365          370          375
ttt tat gcc cct tgg tgt ggt cat tgt aag aac ctg gag ccc aag tat 1365
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
          380          385          390
aaa gaa ctt ggc gag aag ctc agc aaa gac cca aat atc gtc ata gcc 1413
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
          395          400          405
aag atg gat gcc aca gcc aat gat gtg cct tct cca tat gaa gtc aga 1461
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
          410          415          420
ggg ttt cct acc ata tac ttc tct cca gcc aac aag aag cta aat cca 1509
Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
          425          430          435          440
aag aaa tat gaa ggt ggc cgt gaa tta agt gat ttt att agc tat cta 1557
Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
          445          450          455
caa aga gaa gct aca atc ccc cct gta att caa gaa gaa aaa ccc aag 1605
Gln Arg Glu Ala Thr Ile Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
          460          465          470
aag aag aag aag gca cag gag gat ctc taaagcagta gccaaacacc 1652
Lys Lys Lys Lys Ala Gln Glu Asp Leu
          475          480
actttgtaaa aggactcttc catcagagat gggaaaacca ttgggggagga ctaggaccca 1712
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tttaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaawaaaa aaaaaaa 1999

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 <212> PRT
 <213> Homo sapiens

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 <222> 1..24

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 Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
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 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
 10 15 20
 Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
 25 30 35 40
 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
 45 50 55
 Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly

			60					65				70				
Val	Ser	Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Asp	Gly	Glu	Glu	Ala	
		75					80					85				
Gly	Ala	Tyr	Asp	Gly	Pro	Arg	Thr	Ala	Asp	Gly	Ile	Val	Ser	His	Leu	
	90					95					100					
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu	
105					110					115					120	
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe	
			125						130					135		
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser	
			140					145					150			
Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu	
		155					160					165				
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro	
	170					175					180					
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu	
185					190					195					200	
Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile	
			205						210					215		
Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln	
			220					225					230			
Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn	
		235					240					245				
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys	
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265					270					275					280	
Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala	
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Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe	
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Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe	
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Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu	
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Pro	Ile	Pro	Glu	Ser	Asn	Asp	Gly	Pro	Val	Lys	Val	Val	Val	Ala	Glu	
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Asn	Phe	Asp	Glu	Ile	Val	Asn	Asn	Glu	Asn	Lys	Asp	Val	Leu	Ile	Glu	
			365						370					375		
Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Asn	Leu	Glu	Pro	Lys	Tyr	
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Lys	Glu	Leu	Gly	Glu	Lys	Leu	Ser	Lys	Asp	Pro	Asn	Ile	Val	Ile	Ala	
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Lys	Met	Asp	Ala	Thr	Ala	Asn	Asp	Val	Pro	Ser	Pro	Tyr	Glu	Val	Arg	
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Gly	Phe	Pro	Thr	Ile	Tyr	Phe	Ser	Pro	Ala	Asn	Lys	Lys	Leu	Asn	Pro	
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Gln	Arg	Glu	Ala	Thr	Ile	Pro	Pro	Val	Ile	Gln	Glu	Glu	Lys	Pro	Lys	
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 gatgctgtgg ttggatattt agaggacatt atc atg gat gac gag ttc cag tta 174
 Met Asp Asp Glu Phe Gln Leu
 1 5
 tta cag aga aat ttc atg gac aag tac tac ctg gag ttt gaa gac aca 222
 Leu Gln Arg Asn Phe Met Asp Lys Tyr Tyr Leu Glu Phe Glu Asp Thr
 10 15 20
 gaa gag aat aaa ctc atc tac aca cct att ttt aat gaa tac att tct 270
 Glu Glu Asn Lys Leu Ile Tyr Thr Pro Ile Phe Asn Glu Tyr Ile Ser
 25 30 35
 ttg gta gaa aaa tac att gaa gaa cag ctg ctg cag cgg att cct gag 318
 Leu Val Glu Lys Tyr Ile Glu Glu Gln Leu Leu Gln Arg Ile Pro Glu
 40 45 50 55
 ttc aac atg gca gcc ttc acc aca aca tta cag cac cat aag gat gaa 366
 Phe Asn Met Ala Ala Phe Thr Thr Thr Leu Gln His His Lys Asp Glu
 60 65 70
 gtg gct ggt gac ata ttc gac atg ctg ctc acc ttc aca gat ttt ctg 414
 Val Ala Gly Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu
 75 80 85
 gct ttt aaa gaa atg ttt ttg gac tac aga gca gaa aaa gaa ggc cga 462
 Ala Phe Lys Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg
 90 95 100
 gga ctg gac tta agc agt ggc tta gtg gtg act tca ttg tgc aaa tca 510
 Gly Leu Asp Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser
 105 110 115
 tct tct ctg cca gct tcc cag aac aat ctg cgg cac taggtcctac 556
 Ser Ser Leu Pro Ala Ser Gln Asn Asn Leu Arg His
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 ctccagccaa tgaatgggat cattctggat gtcaccagcc caataggctc agtcatgat 616
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 taataggtca aaacccaaat gacctaacc tcctggacct atttcaaaaa aaaaaaaaaa 736

Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile																		
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ggc	gag	atc	gcc	gcc	gcc	gtg	tcc	ttc	atc	tcc	aag	ttt	ctc	cgc	acc	279		
Gly	Glu	Ile	Ala	Ala	Ala	Val	Ser	Phe	Ile	Ser	Lys	Phe	Leu	Arg	Thr			
		15				20				25								
aag	ggg	ctc	acg	agc	gag	cga	cag	ctg	cag	acc	ttc	agc	cag	agc	ctg	327		
Lys	Gly	Leu	Thr	Ser	Glu	Arg	Gln	Leu	Gln	Thr	Phe	Ser	Gln	Ser	Leu			
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Gln	Glu	Leu	Leu	Ala	Glu	His	Tyr	Lys	His	His	Trp	Phe	Pro	Glu	Lys			
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cca	tgc	aag	gga	tcg	ggt	tac	cgt	tgt	att	cgc	atc	aac	cat	aaa	atg	423		
Pro	Cys	Lys	Gly	Ser	Gly	Tyr	Arg	Cys	Ile	Arg	Ile	Asn	His	Lys	Met			
		65				70				75								
gat	cct	ctg	att	gga	cag	gca	gca	cag	cgg	att	gga	ctg	agc	agt	cag	471		
Asp	Pro	Leu	Ile	Gly	Gln	Ala	Ala	Gln	Arg	Ile	Gly	Leu	Ser	Ser	Gln			
		80				85				90								
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Glu	Leu	Phe	Arg	Leu	Leu	Pro	Ser	Glu	Leu	Thr	Leu	Trp	Val	Asp	Pro			
		95				100				105								
tat	gaa	gtg	tcc	tac	aga	att	gga	gag	gat	ggc	tcc	atc	tgt	gtg	ctg	567		
Tyr	Glu	Val	Ser	Tyr	Arg	Ile	Gly	Glu	Asp	Gly	Ser	Ile	Cys	Val	Leu			
		110				115				120								
tat	gaa	gcc	tca	cca	gca	gga	ggt	agc	act	caa	aac	agc	acc	aac	gtg	615		
Tyr	Glu	Ala	Ser	Pro	Ala	Gly	Gly	Ser	Thr	Gln	Asn	Ser	Thr	Asn	Val			
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Gln	Met	Val	Asp	Ser	Arg	Ile	Ser	Cys	Lys	Glu	Glu	Leu	Leu	Leu	Gly			
		145				150				155								
aga	acg	agc	cct	tcc	aaa	aac	tac	aat	atg	atg	act	gta	tca	agt		708		
Arg	Thr	Ser	Pro	Ser	Lys	Asn	Tyr	Asn	Met	Met	Thr	Val	Ser	Ser				
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Ser	Glu	Arg	Gln	Leu	Gln	Thr	Phe	Ser	Gln	Ser	Leu	Gln	Glu	Leu	Leu
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Ala	Glu	His	Tyr	Lys	His	His	Trp	Phe	Pro	Glu	Lys	Pro	Cys	Lys	Gly
	50					55					60				
Ser	Gly	Tyr	Arg	Cys	Ile	Arg	Ile	Asn	His	Lys	Met	Asp	Pro	Leu	Ile
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Gly	Gln	Ala	Ala	Gln	Arg	Ile	Gly	Leu	Ser	Ser	Gln	Glu	Leu	Phe	Arg
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Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Ala Ser
115 120 125
Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val Gln Met Val Asp
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Ser Pro Thr His Ser Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val
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Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg
15 20 25
agc cct ggg cag cat gac ggc acg tac ttc ggg cgg ctg gga atc gca 253
Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
30 35 40
aac cct gcc acg gac ttt cag ttg gaa gtg act cct cag aac att acg 301
Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr
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Val	Leu	Arg	Gln	Asp	Gly	Val	Val	Val	Thr	Ile	Asn	Lys	Lys	Arg	Asn		
			80						85					90			
ctg	gtg	gtg	tct	gtg	gac	gac	ggg	ggc	acc	ttt	gag	gtt	gtt	ttg	cac	445	
Leu	Val	Val	Ser	Val	Asp	Asp	Gly	Gly	Thr	Phe	Glu	Val	Val	Leu	His		
			95						100					105			
cga	gtg	tgg	aag	ggg	agc	tcg	gtc	cac	cag	gac	ttc	ctg	ggc	ttc	tat	493	
Arg	Val	Trp	Lys	Gly	Ser	Ser	Val	His	Gln	Asp	Phe	Leu	Gly	Phe	Tyr		
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Val	Leu	Asp	Ser	His	Arg	Met	Ser	Ala	Arg	Thr	His	Gly	Leu	Leu	Gly		
			125						130					135			
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Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His	Pro	Gly		
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Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn	Arg	Arg		
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ctc	acg	gtc	acc	agg	ggg	ttg	caa	aaa	gac	tac	agc	aag	gac	ccg	tgg	685	
Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp	Pro	Trp		
			175						180					185			
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His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly	Ala	Gly		
			190						195					200			
ctc	atc	gat	ggg	gcc	tac	act	gat	tat	atc	gtc	ccc	gac	atc	ttc		778	
Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile	Phe			
			205						210					215			
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 Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
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 45 50 55
 Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala

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Arg	Val	Trp	Lys	Gly	Ser	Ser	Val	His	Gln	Asp	Phe	Leu	Gly	Phe
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	125					130					135			
Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His	Pro
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Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn	Arg
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Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp	Pro
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His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly	Ala
		190					195					200		
Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile	Phe
	205					210					215			